



PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/856,850A

DATE: 02/14/2002

TIME: 09:36:32

Input Set : A:\1803-279-999.txt

Output Set: N:\CRF3\02142002\I856850A.raw

ENTERED

5 <110> APPLICANT: ANKENBAUER, WALTRAUD  
7 LAUE, FRANK  
9 SOBEK, HERALD  
11 GREIF, MICHAEL  
15 <120> TITLE OF INVENTION: Thermostable Enzyme Promoting The Fidelity Of Thermostable  
DNA  
16 Polymerases - For Improvement Of Nucleic Acid Synthesis And Amplification  
17 In Vitro  
21 <130> FILE REFERENCE: 5304  
25 <140> CURRENT APPLICATION NUMBER: US 09/856,850A  
27 <141> CURRENT FILING DATE: 2001-05-25  
29 <150> PRIOR APPLICATION NUMBER: PCT/EP00/09423  
30 <151> PRIOR FILING DATE: 2000-09-27  
32 <150> PRIOR APPLICATION NUMBER: EP/99119268.3  
33 <151> PRIOR FILING DATE: 1999-09-28  
35 <160> NUMBER OF SEQ ID NOS: 18  
39 <170> SOFTWARE: PatentIn version 3.1  
43 <210> SEQ ID NO: 1  
45 <211> LENGTH: 31  
47 <212> TYPE: DNA  
C--> 49 <213> ORGANISM: Artificial  
51 <220> FEATURE:  
53 <223> OTHER INFORMATION: Amplification Primer  
57 <400> SEQUENCE: 1  
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63 <211> LENGTH: 31  
65 <212> TYPE: DNA  
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71 <220> FEATURE:  
73 <223> OTHER INFORMATION: Amplification Primer  
77 <400> SEQUENCE: 2  
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91 <223> OTHER INFORMATION: Amplification Primer  
95 <400> SEQUENCE: 3  
96 ggttatcgaa atcagccaca gcg 23  
99 <210> SEQ ID NO: 4  
101 <211> LENGTH: 27  
103 <212> TYPE: DNA

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C--> 105 <213> ORGANISM: Artificial
      107 <220> FEATURE:
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      113 <400> SEQUENCE: 4
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      117 <210> SEQ ID NO: 5
      119 <211> LENGTH: 27
      121 <212> TYPE: DNA

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      125 <220> FEATURE:
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      131 <400> SEQUENCE: 5
      132 tggatacgtc tgaactggtc acggtct 27
      135 <210> SEQ ID NO: 6
      137 <211> LENGTH: 27
      139 <212> TYPE: DNA

C--> 141 <213> ORGANISM: Artificial
      143 <220> FEATURE:
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      149 <400> SEQUENCE: 6
      150 tggatacgtc tgaactggtc acggtcc 27
      153 <210> SEQ ID NO: 7
      155 <211> LENGTH: 27
      157 <212> TYPE: DNA

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      161 <220> FEATURE:
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      166 <400> SEQUENCE: 7
      167 tggatacgtc tgaactggtc acggtat 27
      170 <210> SEQ ID NO: 8
      172 <211> LENGTH: 34
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      178 <220> FEATURE:
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      184 <400> SEQUENCE: 8
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214 <220> FEATURE:
216 <223> OTHER INFORMATION: Amplification Primer
220 <400> SEQUENCE: 10
221 tggttgaatt catatatctt agagggaggg c 31
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228 <212> TYPE: DNA
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232 <220> FEATURE:
234 <223> OTHER INFORMATION: Amplification Primer
238 <400> SEQUENCE: 11
239 tgtgtctgca gaaacatca agggctcccat a 31
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246 <212> TYPE: DNA
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250 <220> FEATURE:
252 <223> OTHER INFORMATION: Amplification Primer
256 <400> SEQUENCE: 12
257 ggaagtacag ctcagagttc tgcagcaccc ctgc 34
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264 <212> TYPE: DNA
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268 <220> FEATURE:
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318 <212> TYPE: DNA
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322 <220> FEATURE:

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324 <223> OTHER INFORMATION: Amplification Primer
328 <400> SEQUENCE: 16
329 ccttctagag tcaactctag atgtggactt agag 34
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336 <212> TYPE: DNA
338 <213> ORGANISM: Archaeoglobus fulgidus
342 <220> FEATURE:
344 <221> NAME/KEY: CDS
346 <222> LOCATION: (1)..(774)
348 <223> OTHER INFORMATION:
352 <400> SEQUENCE: 17
353 atg ctc aaa atc gcc acc ttc aac gta aac tcc atc agg agc aga ctg 48
354 Met Leu Lys Ile Ala Thr Phe Asn Val Asn Ser Ile Arg Ser Arg Leu
355 1 5 10 15
357 cac atc gtg att ccg tgg ctg aag gag aac aag cct gac att cta tgc 96
358 His Ile Val Ile Pro Trp Leu Lys Glu Asn Lys Pro Asp Ile Leu Cys
359 20 25 30
361 atg cag gag acg aag gtt gag aac agg aag ttt cct gag gcc gat ttt 144
362 Met Gln Glu Thr Lys Val Glu Asn Arg Lys Phe Pro Glu Ala Asp Phe
363 35 40 45
365 cac cgc atc ggc tac cac gtc gtc ttc agc ggg agc aag gga agg aat 192
366 His Arg Ile Gly Tyr His Val Val Phe Ser Gly Ser Lys Gly Arg Asn
367 50 55 60
369 gga gtg gcc ata gct tcc ctc gaa gag cct gag gat gtc agc ttc ggt 240
370 Gly Val Ala Ile Ala Ser Leu Glu Glu Pro Glu Asp Val Ser Phe Gly
371 65 70 75 80
373 ctc gat tca gag ccg aag gac gag gac agg ctg ata agg gca aag ata 288
374 Leu Asp Ser Glu Pro Lys Asp Glu Asp Arg Leu Ile Arg Ala Lys Ile
375 85 90 95
377 gct ggc ata gac gtg att aac acc tac gtt cct cag gga ttc aaa att 336
378 Ala Gly Ile Asp Val Ile Asn Thr Tyr Val Pro Gln Gly Phe Lys Ile
379 100 105 110
381 gac agc gag aag tac cag tac aag ctc cag tgg ctt gag agg ctt tac 384
382 Asp Ser Glu Lys Tyr Gln Tyr Lys Leu Gln Trp Leu Glu Arg Leu Tyr
383 115 120 125
385 cat tac ctt caa aaa acc gtt gac ttc aga agc ttt gct gtt tgg tgt 432
386 His Tyr Leu Gln Lys Thr Val Asp Phe Arg Ser Phe Ala Val Trp Cys
387 130 135 140
389 gga gac atg aac gtt gct cct gag cca atc gac gtt cac tcc cca gac 480
390 Gly Asp Met Asn Val Ala Pro Glu Pro Ile Asp Val His Ser Pro Asp
391 145 150 155 160
393 aag ctg aag aac cac gtc tgc ttc cac gag gat gcg aga agg gca tac 528
394 Lys Leu Lys Asn His Val Cys Phe His Glu Asp Ala Arg Arg Ala Tyr
395 165 170 175
397 aaa aaa ata ctc gaa ctc ggc ttt gtt gac gtg ctg aga aaa ata cat 576
398 Lys Lys Ile Leu Glu Leu Gly Phe Val Asp Val Leu Arg Lys Ile His
399 180 185 190
401 ccc aac gag aga att tac acc ttc tac gac tac agg gtt aag gga gcc 624

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402 Pro Asn Glu Arg Ile Tyr Thr Phe Tyr Asp Tyr Arg Val Lys Gly Ala
403      195      200      205
405 att gag cgg ggg ctg gga tgg agg gtt gat gcc atc ctc gcc acc cca      672
406 Ile Glu Arg Gly Leu Gly Trp Arg Val Asp Ala Ile Leu Ala Thr Pro
407      210      215      220
409 ccc ctc gcc gaa aga tgc gtg gac tgc tac gca gac atc aaa ccg agg      720
410 Pro Leu Ala Glu Arg Cys Val Asp Cys Tyr Ala Asp Ile Lys Pro Arg
411 225      230      235      240
413 ctg gca gaa aag cca tcc gac cac ctc cct ctc gtt gct gtg ttt gac      768
414 Leu Ala Glu Lys Pro Ser Asp His Leu Pro Leu Val Ala Val Phe Asp
415      245      250      255
417 gtg tag      774
418 Val
422 <210> SEQ ID NO: 18
424 <211> LENGTH: 257
426 <212> TYPE: PRT
428 <213> ORGANISM: Archaeoglobus fulgidus
432 <400> SEQUENCE: 18
434 Met Leu Lys Ile Ala Thr Phe Asn Val Asn Ser Ile Arg Ser Arg Leu
435 1      5      10      15
438 His Ile Val Ile Pro Trp Leu Lys Glu Asn Lys Pro Asp Ile Leu Cys
439      20      25      30
442 Met Gln Glu Thr Lys Val Glu Asn Arg Lys Phe Pro Glu Ala Asp Phe
443      35      40      45
446 His Arg Ile Gly Tyr His Val Val Phe Ser Gly Ser Lys Gly Arg Asn
447      50      55      60
450 Gly Val Ala Ile Ala Ser Leu Glu Glu Pro Glu Asp Val Ser Phe Gly
451 65      70      75      80
454 Leu Asp Ser Glu Pro Lys Asp Glu Asp Arg Leu Ile Arg Ala Lys Ile
455      85      90      95
458 Ala Gly Ile Asp Val Ile Asn Thr Tyr Val Pro Gln Gly Phe Lys Ile
459      100      105      110
462 Asp Ser Glu Lys Tyr Gln Tyr Lys Leu Gln Trp Leu Glu Arg Leu Tyr
463      115      120      125
466 His Tyr Leu Gln Lys Thr Val Asp Phe Arg Ser Phe Ala Val Trp Cys
467      130      135      140
471 Gly Asp Met Asn Val Ala Pro Glu Pro Ile Asp Val His Ser Pro Asp
472 145      150      155      160
475 Lys Leu Lys Asn His Val Cys Phe His Glu Asp Ala Arg Arg Ala Tyr
476      165      170      175
479 Lys Lys Ile Leu Glu Leu Gly Phe Val Asp Val Leu Arg Lys Ile His
480      180      185      190
483 Pro Asn Glu Arg Ile Tyr Thr Phe Tyr Asp Tyr Arg Val Lys Gly Ala
484      195      200      205
487 Ile Glu Arg Gly Leu Gly Trp Arg Val Asp Ala Ile Leu Ala Thr Pro
488      210      215      220
491 Pro Leu Ala Glu Arg Cys Val Asp Cys Tyr Ala Asp Ile Lys Pro Arg
492 225      230      235      240
495 Leu Ala Glu Lys Pro Ser Asp His Leu Pro Leu Val Ala Val Phe Asp

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## VERIFICATION SUMMARY

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Input Set : A:\1803-279-999.txt

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L:49 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1  
L:69 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2  
L:87 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
L:105 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
L:123 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:141 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
L:159 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7  
L:176 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
L:194 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9  
L:212 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10  
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L:248 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12  
L:266 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13  
L:284 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14  
L:302 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15  
L:320 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16